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## RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/10/010,731

TIME: 19:28:34

Input Set : N:\Crf3\RULE60\10010731.txt

Output Set: N:\CRF3\02142002\J010731.raw

## SEQUENCE LISTING

## 2 (1) GENERAL INFORMATION:

(i) APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yonnie S.

Rosenberger, Cindy A.

Hakimi, Salim

(ii) TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold White &amp; Durkee

(B) STREET: P.O. Box 4433

(C) CITY: Houston

(D) STATE: Texas

(E) COUNTRY: USA

(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/010,731

(B) FILING DATE: 13-Nov-2001

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/003,198

(B) FILING DATE: 07-JAN-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Patterson, Melinda L.

(B) REGISTRATION NUMBER: 33,062

(C) REFERENCE/DOCKET NUMBER: MOBT:193

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (713) 787-1400

(B) TELEFAX: (713) 787-1440

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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48   Arg Thr Cys Glu Asn Leu Ala Asp Lys Tyr Arg Gly Pro Cys Phe Ser
49   1             5             10             15
50   Gly Cys Asp Thr His Cys Thr Thr Lys Glu Asn Ala Val Ser Gly Arg
51             20             25             30
W--> 52   Cys Arg Asp Asp Phe Arg Cys Xaa Xaa Thr Lys
53             35             40
54 (2) INFORMATION FOR SEQ ID NO: 2:
55   (i) SEQUENCE CHARACTERISTICS:
56       (A) LENGTH: 45 amino acids
57       (B) TYPE: amino acid
58       (C) STRANDEDNESS:
59       (D) TOPOLOGY: linear
60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
61   Arg Thr Cys Glu Asn Leu Ala Asp Lys Tyr Arg Gly Pro Cys Phe Ser
62   1             5             10             15
63   Gly Cys Asp Thr His Cys Thr Thr Lys Glu Asn Ala Val Ser Gly Arg
64             20             25             30
65   Cys Arg Asp Asp Phe Arg Cys Trp Cys Thr Lys Arg Cys
66             35             40             45
67 (2) INFORMATION FOR SEQ ID NO: 3:
68   (i) SEQUENCE CHARACTERISTICS:
69       (A) LENGTH: 33 base pairs
70       (B) TYPE: nucleic acid
71       (C) STRANDEDNESS: single
72       (D) TOPOLOGY: linear
73   (ix) FEATURE:
74       (A) NAME/KEY: modified_base
75       (B) LOCATION: one-of(16, 22)
76       (D) OTHER INFORMATION: /mod_base= OTHER
77 /note= "N = inosine"
78   (ix) FEATURE:
79       (A) NAME/KEY: modified_base
80       (B) LOCATION: one-of(19, 25, 28, 31)
81       (D) OTHER INFORMATION: /mod_base= OTHER
82 /note= "D = A or G or T"
83   (ix) FEATURE:
84       (A) NAME/KEY: modified_base
85       (B) LOCATION: 24
86       (D) OTHER INFORMATION: /mod_base= OTHER
87 /note= "K = G or T"
88   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89 GGGAATTCGG ATCCANCADC ANCKDAADTC DTC
90 (2) INFORMATION FOR SEQ ID NO: 4:
91   (i) SEQUENCE CHARACTERISTICS:
92       (A) LENGTH: 30 base pairs
93       (B) TYPE: nucleic acid
94       (C) STRANDEDNESS: single
95       (D) TOPOLOGY: linear
96   (ix) FEATURE:

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97      (A) NAME/KEY: modified_base
98      (B) LOCATION: join(18..19, 23..24, 28..29)
99      (D) OTHER INFORMATION: /mod_base= OTHER
100 /note= "N = inosine"
101      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
102 GGGGAATTCGG ATCCGGGNGG GGNNGGGNNG                      30
103 (2) INFORMATION FOR SEQ ID NO: 5:
104      (i) SEQUENCE CHARACTERISTICS:
105          (A) LENGTH: 200 base pairs
106          (B) TYPE: nucleic acid
107          (C) STRANDEDNESS: double
108          (D) TOPOLOGY: linear
109      (ix) FEATURE:
110          (A) NAME/KEY: modified_base
111          (B) LOCATION: 17
112          (D) OTHER INFORMATION: /mod_base= OTHER
113 /note= "N = A or C or G or T"
114      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
115 GGGGGGGGGG GGGGGGNCAG GCTTATGCTT CCTCTTCTTG GTTCTCTTTG TTGCACAAGA      60
116 AATTGTGGTG ACAGAAGCCA GAACATGTGA GAATTTGGCA GATAAATATA GGGGACCATG      120
117 CTTTAGTGGT TGTGACACTC ACTGCACAAC CAAAGAGAAC GCAGTTAGTG GAAGGTGTAG      180
118 GGACGACTTC CGCTGCTGCT                      200
119 (2) INFORMATION FOR SEQ ID NO: 6:
120      (i) SEQUENCE CHARACTERISTICS:
121          (A) LENGTH: 293 base pairs
122          (B) TYPE: nucleic acid
123          (C) STRANDEDNESS: double
124          (D) TOPOLOGY: linear
125      (ix) FEATURE:
126          (A) NAME/KEY: modified_base
127          (B) LOCATION: one-of(17, 265)
128          (D) OTHER INFORMATION: /mod_base= OTHER
129 /note= "N = A or C or G or T"
130      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
131 GGGGGGGGGG GGGGGGNTGT CAAACACACA CATAACACAT AAGTGACCGT GAGTCATTAA      60
132 ATTTATATAT ATTCATCAAT CTAATCAAAC TATGGAGAAG AAATCACTAG CTGGCTTATG      120
133 CTTCTCTTTC CTCGTTCTCT TTGTTGAACA AGAAATTATG GTGACCGAGG CAGCTACTTG      180
134 TGAGAATTTG GCTAACACAT ACAGGGGACC ATGCTTCGGT GGTGTGACT TTTACTGCAA      240
135 AACCAAAGAA CACTTACTTA GCGGNAGGTG CAGGGACGAC TTCCGCTGCT GCT          293
136 (2) INFORMATION FOR SEQ ID NO: 7:
137      (i) SEQUENCE CHARACTERISTICS:
138          (A) LENGTH: 33 base pairs
139          (B) TYPE: nucleic acid
140          (C) STRANDEDNESS: single
141          (D) TOPOLOGY: linear
142      (ix) FEATURE:
143          (A) NAME/KEY: modified_base
144          (B) LOCATION: one-of(17, 31)
145          (D) OTHER INFORMATION: /mod_base= OTHER

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146 /note= "D = A or G or T"
147     (ix) FEATURE:
148         (A) NAME/KEY: modified_base
149         (B) LOCATION: one-of(19, 20, 28)
150         (D) OTHER INFORMATION: /mod_base= OTHER
151 /note= "B = C or G or T"
152     (ix) FEATURE:
153         (A) NAME/KEY: modified_base
154         (B) LOCATION: one-of(22, 25)
155         (D) OTHER INFORMATION: /mod_base= OTHER
156 /note= "N = inosine"
157     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
158 GCGAATTCGG ATCCGADABB TNGCNGABAA DTA 33
159 (2) INFORMATION FOR SEQ ID NO: 8:
160     (i) SEQUENCE CHARACTERISTICS:
161         (A) LENGTH: 32 base pairs
162         (B) TYPE: nucleic acid
163         (C) STRANDEDNESS: single
164         (D) TOPOLOGY: linear
165     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
166 GCGAATTCGG ATCCTTTTTT TTTTTTTTTT TT 32
167 (2) INFORMATION FOR SEQ ID NO: 9:
168     (i) SEQUENCE CHARACTERISTICS:
169         (A) LENGTH: 327 base pairs
170         (B) TYPE: nucleic acid
171         (C) STRANDEDNESS: double
172         (D) TOPOLOGY: linear
173     (ix) FEATURE:
174         (A) NAME/KEY: modified_base
175         (B) LOCATION: one-of(244, 305)
176         (D) OTHER INFORMATION: /mod_base= OTHER
177 /note= "N = A or C or G or T"
178     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
179 GAGAATTTGG CGGATAAGTA TAGGGGACCA TGCTTTAGTG GTTGTGACAC TCACTGCACA 60
180 ACCAAAGAGA ACGCAGTTAG TGGAAGGTGT AGGGATGACT TTCGTTGTTA GTGTACTAAA 120
181 AGATGTTAAA TGGATCTCCT CCAACATCAA GATGTGCATG GAATAGTCTT TATAATAAAA 180
182 CTAAATAAAT AAAATGCACG CAGTATAGCT ACAACTTCAT CTATATATAT GTACTCAATA 240
183 TCGNGCATAA CGTATTAGTT ATGCACTTCT ATCATATGGA ATAAACATCA ATAAGTAATT 300
184 TCGTNTCCAA AAAAAAAAAA AAAAAAAA 327
185 (2) INFORMATION FOR SEQ ID NO: 10:
186     (i) SEQUENCE CHARACTERISTICS:
187         (A) LENGTH: 507 base pairs
188         (B) TYPE: nucleic acid
189         (C) STRANDEDNESS: double
190         (D) TOPOLOGY: linear
191     (ix) FEATURE:
192         (A) NAME/KEY: modified_base
193         (B) LOCATION: one-of(17, 424, 485)
194         (D) OTHER INFORMATION: /mod_base= OTHER

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195 /note= "N = A or C or G or T"

196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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197 GGGGGGGGGG GGGGGGNTGT CAAACACACA CATAACACAT AAGTGACCGT GAGTCATTAA      60
198 ATTTATATAT ATTCATCAAT CTAATCAAAC TATGGAGAAG AAATCACTAG CTGGCTTATG      120
199 CTCCTCTTCT TTGGTTCTCT TTGTTGCACA AGAAATTGTG GTGACAGAAG CCAGAACATG      180
200 TGAGAATTTG GCAGATAAAT ATAGGGGACC ATGCTTTAGT GGTGTGACA CTCACTGCAC      240
201 AACCAAAGAG AACGCAGTTA GTGGAAGGTG TAGGGACGAC TTCCGCTGCT GGTGTACTAA      300
202 AAGATGTTAA ATGGATCTCC TCCAACATCA AGATGTGCAT GGAATAGTCT TTATAATAAA      360
203 ACTAAATAAA TAAAATGCAC GCAGTATAGC TACAACTTCA TCTATATATA TGACTIONA      420
204 TCGNGCATAA CGTATTAGTT ATGCACTTCT ATCATATGGA ATAAACATCA ATAAGTAATT      480
205 TCGTNTCCAA AAAAAAAAAA AAAAAAA      507

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206 (2) INFORMATION FOR SEQ ID NO: 11:

207 (i) SEQUENCE CHARACTERISTICS:

```

208 (A) LENGTH: 62 base pairs
209 (B) TYPE: nucleic acid
210 (C) STRANDEDNESS: single
211 (D) TOPOLOGY: linear

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212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

213 GGGGATCCCA ATCTAATCAA ACTATGGAGA AGAAATCACT AGCTGGCTTA TGCTTCCTCT      60
214 TC      62

```

215 (2) INFORMATION FOR SEQ ID NO: 12:

216 (i) SEQUENCE CHARACTERISTICS:

```

217 (A) LENGTH: 47 base pairs
218 (B) TYPE: nucleic acid
219 (C) STRANDEDNESS: single
220 (D) TOPOLOGY: linear

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221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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222 GGGGATCCTT AACATCTTTT AGTACACCAG CAGCGGAAGT CGTCCCT      47

```

223 (2) INFORMATION FOR SEQ ID NO: 13:

224 (i) SEQUENCE CHARACTERISTICS:

```

225 (A) LENGTH: 250 base pairs
226 (B) TYPE: nucleic acid
227 (C) STRANDEDNESS: double
228 (D) TOPOLOGY: linear

```

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

230 GGGGATCCCA ATCTAATCAA ACTATGGAGA AGAAATCACT AGCTGGCTTA TGCTTCCTCT      60
231 TCTTGTTTCT CTTTGTGCA CAAGAAATTG TGGTGACAGA AGCCAGAACA TGTGAGAATT      120
232 TGGCAGATAA ATATAGGGGA CCATGCTTTA GTGGTTGTGA CACTCACTGC ACAACCAAAG      180
233 AGAACGCAGT TAGTGGAAGG TGTAGGGACG ACTTCCGCTG CTGGTGTACT AAAAGATGTT      240
234 AAGGATCCCC      250

```

235 (2) INFORMATION FOR SEQ ID NO: 14:

236 (i) SEQUENCE CHARACTERISTICS:

```

237 (A) LENGTH: 40 amino acids
238 (B) TYPE: amino acid
239 (C) STRANDEDNESS:
240 (D) TOPOLOGY: linear

```

241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

242 Ala Thr Cys Glu Asn Leu Ala Asn Thr Tyr Arg Gly Pro Cys Phe Gly
243 1 5 10 15

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VERIFICATION SUMMARY

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DATE: 02/14/2002

TIME: 19:28:35

Input Set : N:\Crf3\RULE60\10010731.txt

Output Set: N:\CRF3\02142002\J010731.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1